

p#18



1642

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1600

RAW SEQUENCE LISTING

DATE: 04/12/2002

PATENT APPLICATION: US/09/581,651A

TIME: 14:21:03

Input Set : A:\350013-72.txt

Output Set: N:\CRF3\04122002\I581651A.raw

4 <110> APPLICANT: Schor, Seth Laurence
 5 Schor, Ana Maria
 7 <120> TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND USES
 8 THEREOF
 10 <130> FILE REFERENCE: 350013-72
 12 <140> CURRENT APPLICATION NUMBER: 09/581,651A
 13 <141> CURRENT FILING DATE: 2000-10-10
 15 <160> NUMBER OF SEQ ID NOS: 15
 17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 660
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Human
 24 <400> SEQUENCE: 1

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 TECH CENTER 1600/2900

25 Asn Leu Val Ala Thr Cys Leu Pro Val Arg Ala Ser Leu Pro His Arg
 26 1 5 10 15
 27 Leu Asn Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val
 28 20 25 30
 29 Gln Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys
 30 35 40 45
 31 Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser
 32 50 55 60
 33 Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn
 34 65 70 75 80
 35 Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys
 36 85 90 95
 37 Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu
 38 100 105 110
 39 Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp
 40 115 120 125
 41 Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile
 42 130 135 140
 43 Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His
 44 145 150 155 160
 45 Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His
 46 165 170 175
 47 Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys
 48 180 185 190
 49 Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala
 50 195 200 205
 51 Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln
 52 210 215 220
 53 Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg

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54	225				230				235				240			
55	Ile	Thr	Cys	Thr	Ser	Arg	Asn	Arg	Cys	Asn	Asp	Gln	Asp	Thr	Arg	Thr
56					245				250						255	
57	Ser	Tyr	Arg	Ile	Gly	Asp	Thr	Trp	Ser	Lys	Lys	Asp	Asn	Arg	Gly	Asn
58				260					265						270	
59	Leu	Leu	Gln	Cys	Ile	Cys	Thr	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Lys	Cys
60			275					280					285			
61	Glu	Arg	His	Thr	Ser	Val	Gln	Thr	Thr	Ser	Ser	Gly	Ser	Gly	Pro	Phe
62		290					295					300				
63	Thr	Asp	Val	Arg	Ala	Ala	Val	Tyr	Gln	Pro	Gln	Pro	His	Pro	Gln	Pro
64	305				310						315					320
65	Pro	Pro	Tyr	Gly	His	Cys	Val	Thr	Asp	Ser	Gly	Val	Val	Tyr	Ser	Val
66				325						330					335	
67	Gly	Met	Gln	Trp	Leu	Lys	Thr	Gln	Gly	Asn	Lys	Gln	Met	Leu	Cys	Thr
68			340						345					350		
69	Cys	Leu	Gly	Asn	Gly	Val	Ser	Cys	Gln	Glu	Thr	Ala	Val	Thr	Gln	Thr
70			355					360					365			
71	Tyr	Gly	Gly	Asn	Ser	Asn	Gly	Glu	Pro	Cys	Val	Leu	Pro	Phe	Thr	Tyr
72		370					375					380				
73	Asn	Asp	Arg	Thr	Asp	Ser	Thr	Thr	Ser	Asn	Tyr	Glu	Gln	Asp	Gln	Lys
74	385					390					395					400
75	Tyr	Ser	Phe	Cys	Thr	Asp	His	Thr	Val	Leu	Val	Gln	Thr	Arg	Gly	Gly
76				405						410					415	
77	Asn	Ser	Asn	Gly	Ala	Leu	Cys	His	Phe	Pro	Phe	Leu	Tyr	Asn	Asn	His
78			420						425					430		
79	Asn	Tyr	Thr	Asp	Cys	Thr	Ser	Glu	Gly	Arg	Arg	Asp	Asn	Met	Lys	Trp
80		435						440					445			
81	Cys	Gly	Thr	Thr	Gln	Asn	Tyr	Asp	Ala	Asp	Gln	Lys	Phe	Gly	Phe	Cys
82		450					455					460				
83	Pro	Met	Ala	Ala	His	Glu	Glu	Ile	Cys	Thr	Thr	Asn	Glu	Gly	Val	Met
84	465				470						475					480
85	Tyr	Arg	Ile	Gly	Asp	Gln	Trp	Asp	Lys	Gln	His	Asp	Met	Gly	His	Met
86				485						490					495	
87	Met	Arg	Cys	Thr	Cys	Val	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Thr	Cys	Ile
88			500						505					510		
89	Ala	Tyr	Ser	Gln	Leu	Arg	Asp	Gln	Cys	Ile	Val	Asp	Asp	Ile	Thr	Tyr
90			515					520					525			
91	Asn	Val	Asn	Asp	Thr	Phe	His	Lys	Arg	His	Glu	Glu	Gly	His	Met	Leu
92		530					535					540				
93	Asn	Cys	Thr	Cys	Phe	Gly	Gln	Gly	Arg	Gly	Arg	Trp	Lys	Cys	Asp	Pro
94	545				550					555					560	
95	Val	Asp	Gln	Cys	Gln	Asp	Ser	Glu	Thr	Gly	Thr	Phe	Tyr	Gln	Ile	Gly
96				565						570					575	
97	Asp	Ser	Trp	Glu	Lys	Tyr	Val	His	Gly	Val	Arg	Tyr	Gln	Cys	Tyr	Cys
98			580						585					590		
99	Tyr	Gly	Arg	Gly	Ile	Gly	Glu	Trp	His	Cys	Gln	Pro	Leu	Gln	Thr	Tyr
100			595					600					605			
101	Pro	Ser	Ser	Ser	Gly	Pro	Val	Glu	Val	Phe	Ile	Thr	Glu	Thr	Pro	Ser
102		610					615						620			

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103  Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His
104  625                               630                               635                               640
105  Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg
106                               645                               650                               655
107  Asn Leu Gly Tyr
108                               660
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 2147
112 <212> TYPE: DNA
113 <213> ORGANISM: Human
115 <400> SEQUENCE: 2
116  caaacttggt ggcaacttgc ctcccgggtgc gggcgtctct ccccccacgt ctcaacatgc      60
117  ttaggggtcc ggggcccggg ctgctgctgc tggcctgcc gtgcctggg acagcgggtgc      120
118  cctccacggg agcctcgaag agcaagaggc aggcctagca aatgggtcag cccaggtccc      180
119  cggtggtgtg cagtcaaagc aagccgggtt gttatgacaa tggaaaacac tatcagataa      240
120  atcaacagtg ggagcggacc tacctaggca atgcgttggt ttgtacttgt tatggaggaa      300
121  gccgaggttt taactgcgag agtaaacctg aagctgaaga gacttgcttt gacaagtaca      360
122  ctgggaacac ttaccgagtg ggtgacactt atgagcgtcc taaagactcc atgatctggg      420
123  actgtacctg catcggggct gggcgaggga gaataagctg taccatcgca aaccgctgcc      480
124  atgaaggggg tcagtcctac aagattgggt acacctggag gagaccacat gagactggtg      540
125  gttacatgtt agagtgtgtg tgtcttggtg atggaaaagg agaattggacc tgcaagccca      600
126  tagctgagaa gtgttttgat catgctgctg ggacttccta tgtggtcgga gaaacgtggg      660
127  agaagcccta ccaaggctgg atgatggtag attgtacttg cctgggagaa ggcagcggac      720
128  gcatcacttg cacttctaga aatagatgca acgatcagga cacaaggaca tcctatagaa      780
129  ttggagacac ctggagcaag aaggataatc gaggaaacct gctccagtgc atctgcacag      840
130  gcaacggccg aggagagtgg aagtgtgaga ggcacacctc tgtgcagacc acatcgagcg      900
131  gatctggccc cttcaccgat gttcgtgcag ctgtttacca accgcagcct cccccccagc      960
132  ctctcccta tggccactgt gtcacagaca gtggtgtggt ctactctgtg gggatgcagt      1020
133  ggctgaagac acaaggaaat aagcaaatgc ttgacagtg cctgggcaac ggagtcagct      1080
134  gccaaagagc agctgtaacc cagacttacg gtggcaactc aaatggagag ccattgtgtc      1140
135  taccattcac ctacaacgac aggacggaca gcacaacttc gaattatgag caggaccaga      1200
136  aatactcttt ctgcacagac cacactgttt tggttcagac tcgaggagga aattccaatg      1260
137  gtgccttggt ccacttcccc ttctatata acaaccacaa ttactatgat tgcacttctg      1320
138  agggcagaag agacaacatg aagtgggtgt ggaccacaca gaactatgat gccgaccaga      1380
139  agtttggttt ctgccccatg gctgcccacg aggaaatctg cacaaccaat gaaggggtca      1440
140  tgtaccgcat tggagatcag tgggataagc agcatgacat gggtcacatg atgaggtgca      1500
141  cgtgtgttgg gaatggtcgt ggggaatgga catgcattgc ctactcgcag cttcgagatc      1560
142  agtgcattgt tgatgacatc acttacaatg tgaacgacac attccacaag cgtcatgaag      1620
143  aggggcacat gctgaactgt acatgcttcg gtcagggtcg gggcaggtgg aagtgtgac      1680
144  ccgtcgacca atgccaggat tcagagactg ggacgtttta tcaaattgga gattcatggg      1740
145  agaagtatgt gcatggtgtc agataccagt gctactgcta tggccgtggc attggggagt      1800
146  ggcatcgcca acctttacag acctatccaa gctcaagtgg tcctgtcgaa gtatttatca      1860
147  ctgagactcc gagtcagccc aactcccacc ccacccagtg gaatgcacca cagccatctc      1920
148  acatttccaa gtacattctc aggtggagac ctgtgagtat cccaccaga aaccttggat      1980
149  actgagtctc ctaattctat caattctgat ggtttctttt ttccccagct tttagccaa      2040
150  caactctgat taactattcc tatagcattt actatatttg tttagtgaac aaacaatatg      2100
151  tggteaatta aattgacttg tagactgaaa aaaaaaaaaa aaaaaaa      2147
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 20

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155 <212> TYPE: PRT
156 <213> ORGANISM: Human
158 <400> SEQUENCE: 3
159 Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg
160 1 5 10 15
161 Asn Leu Gly Tyr
162 20
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 21
166 <212> TYPE: PRT
167 <213> ORGANISM: Human
169 <400> SEQUENCE: 4
170 Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys
171 1 5 10 15
172 Tyr Gly Gly Ser Arg
173 20
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 23
177 <212> TYPE: PRT
178 <213> ORGANISM: Human
180 <400> SEQUENCE: 5
181 Pro Cys Val Leu Pro Phe Thr Tyr Asn Asp Arg Thr Asp Ser Thr Thr
182 1 5 10 15
183 Ser Asn Tyr Glu Gln Asp Gln
184 20
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 20
188 <212> TYPE: PRT
189 <213> ORGANISM: Human
191 <400> SEQUENCE: 6
192 Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn Gly
193 1 5 10 15
194 Ala Leu Cys His
195 20
197 <210> SEQ ID NO: 7
198 <211> LENGTH: 21
199 <212> TYPE: PRT
200 <213> ORGANISM: Human
202 <400> SEQUENCE: 7
203 Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser Gln Leu
204 1 5 10 15
205 Arg Asp Gln Cys Ile
206 20
208 <210> SEQ ID NO: 8
209 <211> LENGTH: 21
210 <212> TYPE: PRT
211 <213> ORGANISM: Human
213 <400> SEQUENCE: 8
214 Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys

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215      1              5              10              15
216 Tyr Gly Gly Ser Arg
217              20
219 <210> SEQ ID NO: 9
220 <211> LENGTH: 39
221 <212> TYPE: PRT
222 <213> ORGANISM: Human
224 <400> SEQUENCE: 9
225 Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser
226      1              5              10              15
227 Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu Trp Cys Ser Thr Thr
228              20              25              30
229 Ser Asn Tyr Glu Gln Asp Gln
230              35
232 <210> SEQ ID NO: 10
233 <211> LENGTH: 21
234 <212> TYPE: PRT
235 <213> ORGANISM: Human
237 <400> SEQUENCE: 10
238 Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly Gly Asn Ser Asn
239      1              5              10              15
240 Gly Ala Leu Cys His
241              20
243 <210> SEQ ID NO: 11
244 <211> LENGTH: 21
245 <212> TYPE: PRT
246 <213> ORGANISM: Human
248 <400> SEQUENCE: 11
249 Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Tyr Ala Tyr Ser Gln Leu
250      1              5              10              15
251 Arg Asp Gln Cys Ile
252              20
254 <210> SEQ ID NO: 12
255 <211> LENGTH: 20
256 <212> TYPE: PRT
257 <213> ORGANISM: Human
259 <400> SEQUENCE: 12
260 Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg
261      1              5              10              15
262 Trp Lys Glu Ala
263              20
265 <210> SEQ ID NO: 13
266 <211> LENGTH: 11
267 <212> TYPE: PRT
268 <213> ORGANISM: Human
270 <400> SEQUENCE: 13
271 Thr Ala Ser Gly Val Ala Glu Thr Thr Asn Cys
272      1              5              10
274 <210> SEQ ID NO: 14

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VERIFICATION SUMMARY

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